STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/069,772 A*
Source: *TEUNO*
Date Processed by STIC: *2/24/06*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
    http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
    U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/069,772 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa

"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFW**0**

```
RAW SEQUENCE LISTING                    DATE: 02/24/2006
PATENT APPLICATION:  US/10/069,772A     TIME: 15:43:05

     Input Set : F:\Feussner-10069772-060211-SEQLIST.txt
     Output Set: N:\CRF4\02242006\J069772A.raw

  3 <110> APPLICANT: Feussner, Ivo
  4         Hornung, Ellen
  5         Fritsche, Kathrin
  6         Peitzsch, Nicola
  8 <120> TITLE OF INVENTION: Fatty acid desaturase gene from plants
 10 <130> FILE REFERENCE: 50669
 12 <140> CURRENT APPLICATION NUMBER: US 10/069,772A
 13 <141> CURRENT FILING DATE: 2002-02-28
 15 <160> NUMBER OF SEQ ID NOS: 16
 17 <170> SOFTWARE: PatentIn version 3.3
```

ol5

Dces Not Comply
Corrected Diskette Needed
(pg. 1, 4-7)

```
RORED SEQUENCES

 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1285
 21 <212> TYPE: DNA
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (42)..(1175)
-> 27 <213> ORGANISM:
-> 27 <400> SEQUENCE: 1
 28 aaaagctcac ttctctgtga gggtaattat atatcaacaa c atg ggt gct ggt ggt   56
 29                                              Met Gly Ala Gly Gly
 30                                                1               5
 32 cgg atg tcg gat cca tct gag gga aaa aac atc ctt gaa cgt gtg cca  104
 33 Arg Met Ser Asp Pro Ser Glu Gly Lys Asn Ile Leu Glu Arg Val Pro
 34             10                  15                  20
 37 gtc gat cca ccg ttc acg tta agc gat ctg aag aaa gcg att cct acc  152
 38 Val Asp Pro Pro Phe Thr Leu Ser Asp Leu Lys Lys Ala Ile Pro Thr
 39             25                  30                  35
 41 cat tgc ttt gag cga tct gtc atc cgg tca tca tac tat gtt gtt cat  200
 42 His Cys Phe Glu Arg Ser Val Ile Arg Ser Ser Tyr Tyr Val Val His
 43             40                  45                  50
 45 gat ctc att gtt gcc tat gtc ttc tac tac ctt gca aac acg tat atc  248
 46 Asp Leu Ile Val Ala Tyr Val Phe Tyr Tyr Leu Ala Asn Thr Tyr Ile
 47         55                  60                  65
 49 cct ctt att cct aca cct ctg gct tac cta gca tgg ccc gtt tac tgg  296
 50 Pro Leu Ile Pro Thr Pro Leu Ala Tyr Leu Ala Trp Pro Val Tyr Trp
 51 70                  75                  80                  85
 53 ttt tgt caa gct agc atc ctc acc ggc ctc tgg gtc atc ggt cac gaa  344
 54 Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu
 55                 90                  95                  100
 57 tgt ggt cac cat gca ttt agc gac tac cag ttg att gat gac att gtt  392
```

Insert here ← See item #11 on error summary sheet. pls insert this mandatory numeric identifier

pls insert <220> whenever <221>, <222>, <223> is present.

```
58 Cys Gly His His Ala Phe Ser Asp Tyr Gln Leu Ile Asp Asp Ile Val
59          105               110             115
61 gga ttc gtg ctc cat tcg gct ctc ctc acc ccg tat ttc tct tgg aaa   440
62 Gly Phe Val Leu His Ser Ala Leu Leu Thr Pro Tyr Phe Ser Trp Lys
63          120               125             130
65 tat agc cac agg aat cac cac gcc aac aca aat tca ctc gat aac gat   488
67 Tyr Ser His Arg Asn His His Ala Asn Thr Asn Ser Leu Asp Asn Asp
68       135               140               145
70 gaa gtt tac att cct aaa cgt aag tcg aag gtc aag att tat tcc aaa   536
71 Glu Val Tyr Ile Pro Lys Arg Lys Ser Lys Val Lys Ile Tyr Ser Lys
72 150             155               160               165
74 ctt ctt aac aat cca ccc ggg cga gtg ttc act ttg gtg ttt cgg ttg   584
75 Leu Leu Asn Asn Pro Pro Gly Arg Val Phe Thr Leu Val Phe Arg Leu
76             170               175             180
78 act tta gga ttt ccg tta tac ctc tta act aat atc tcg ggc aag aaa   632
79 Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile Ser Gly Lys Lys
80          185               190             195
82 tac ggg agg ttt gcc aac cac ttt gat ccc atg agt cca att ttc aac   680
83 Tyr Gly Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Asn
84          200               205             210
86 gat cgt gaa cgc gtt caa gtt ttg cta tcc gat ttc ggt ctt ctc gct   728
87 Asp Arg Glu Arg Val Gln Val Leu Leu Ser Asp Phe Gly Leu Leu Ala
88       215               220               225
90 gta ttt tat gca atc aag ctt ctt gta gca gca aaa ggg gca gct tgg   776
91 Val Phe Tyr Ala Ile Lys Leu Leu Val Ala Ala Lys Gly Ala Ala Trp
92 230             235               240               245
94 gta atc aac atg tac gca att cca gta cta ggt gta agc gtg ttc ttc   824
95 Val Ile Asn Met Tyr Ala Ile Pro Val Leu Gly Val Ser Val Phe Phe
96             250               255             260
99 gtt ttg atc aca tat ttg cac cac acc cat ctc tca ctc cct cat tat   872
100 Val Leu Ile Thr Tyr Leu His His Thr His Leu Ser Leu Pro His Tyr
101             265               270             275
103 gat tca acc gaa tgg aac tgg atc aaa ggc gcc tta tca aca atc gat   920
104 Asp Ser Thr Glu Trp Asn Trp Ile Lys Gly Ala Leu Ser Thr Ile Asp
105          280               285             290
107 agg gat ttc ggg ttc ctg aat cgg gtt ttc cac gac gtt aca cac act   968
108 Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His Asp Val Thr His Thr
109          295               300             305
111 cac gtc ttg cat cat ttg atc tca tac att cca cat tat cat gca aag  1016
112 His Val Leu His His Leu Ile Ser Tyr Ile Pro His Tyr His Ala Lys
113 310             315               320               325
115 gaa gca agg gat gca atc aag cca gtg ttg ggc gag tac tat aaa atc  1064
116 Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly Glu Tyr Tyr Lys Ile
117             330               335             340
119 gac agg act cca att ttc aaa gca atg tat aga gag gct aag gaa tgc  1112
120 Asp Arg Thr Pro Ile Phe Lys Ala Met Tyr Arg Glu Ala Lys Glu Cys
121          345               350             355
123 atc tac atc gag ccc gat gag gat agc gag cac aaa ggt gtg ttc tgg  1160
124 Ile Tyr Ile Glu Pro Asp Glu Asp Ser Glu His Lys Gly Val Phe Trp
```

```
125         360                365                370
127 tac cac aag atg taa tcaaaaaggt gtatgtcaat gcaattgtat gcttaattaa   1215
128 Tyr His Lys Met
130         375
132 gttgttaaac tttctattcc gtgtaataaa ttatcattaa gagaaaaaaa aaaaaaaaaa 1275
134 aaaaaaaaaa                                     .                   1285
137 <210> SEQ ID NO: 2
138 <211> LENGTH: 377
139 <212> TYPE: PRT
140 <213> ORGANISM: Calendula officinalis
143 <400> SEQUENCE: 2
144 Met Gly Ala Gly Gly Arg Met Ser Asp Pro Ser Glu Gly Lys Asn Ile
145   1               5                 10                15
147 Leu Glu Arg Val Pro Val Asp Pro Pro Phe Thr Leu Ser Asp Leu Lys
148             20              25              30
150 Lys Ala Ile Pro Thr His Cys Phe Glu Arg Ser Val Ile Arg Ser Ser
151         35              40              45
153 Tyr Tyr Val Val His Asp Leu Ile Val Ala Tyr Val Phe Tyr Tyr Leu
154     50              55              60
156 Ala Asn Thr Tyr Ile Pro Leu Ile Pro Thr Pro Leu Ala Tyr Leu Ala
157 65              70              75              80
159 Trp Pro Val Tyr Trp Phe Cys Gln Ala Ser Ile Leu Thr Gly Leu Trp
160             85              90              95
163 Val Ile Gly His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Leu
164         100             105             110
166 Ile Asp Asp Ile Val Gly Phe Val Leu His Ser Ala Leu Leu Thr Pro
167         115             120             125
169 Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn
170     130             135             140
172 Ser Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Arg Lys Ser Lys Val
173 145             150             155             160
175 Lys Ile Tyr Ser Lys Leu Leu Asn Asn Pro Pro Gly Arg Val Phe Thr
176             165             170             175
178 Leu Val Phe Arg Leu Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn
179             180             185             190
181 Ile Ser Gly Lys Lys Tyr Gly Arg Phe Ala Asn His Phe Asp Pro Met
182         195             200             205
184 Ser Pro Ile Phe Asn Asp Arg Glu Arg Val Gln Val Leu Leu Ser Asp
185     210             215             220
187 Phe Gly Leu Leu Ala Val Phe Tyr Ala Ile Lys Leu Leu Val Ala Ala
188 225             230             235             240
190 Lys Gly Ala Ala Trp Val Ile Asn Met Tyr Ala Ile Pro Val Leu Gly
191             245             250             255
194 Val Ser Val Phe Phe Val Leu Ile Thr Tyr Leu His His Thr His Leu
195             260             265             270
197 Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Lys Gly Ala
198         275             280             285
200 Leu Ser Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His
201         290             295             300
```

RAW SEQUENCE LISTING   DATE: 02/24/2006
PATENT APPLICATION: **US/10/069,772A**   TIME: 15:43:05

Input Set : **F:\Feussner-10069772-060211-SEQLIST.txt**
Output Set: **N:\CRF4\02242006\J069772A.raw**

```
203 Asp Val Thr His Thr His Val Leu His His Leu Ile Ser Tyr Ile Pro
204 305             310             315             320
206 His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly
207             325             330             335
209 Glu Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Phe Lys Ala Met Tyr Arg
210             340             345             350
212 Glu Ala Lys Glu Cys Ile Tyr Ile Glu Pro Asp Glu Asp Ser Glu His
213             355             360             365
215 Lys Gly Val Phe Trp Tyr His Lys Met
216     370             375
```
-> 219   SEQUENCE LISTING
-> 221 <110> APPLICANT: Feussner, Ivo
-> 221 <110> APPLICANT: Feussner, Ivo
-> 226 <120> TITLE OF INVENTION: Fatty acid desaturase gene from plants
-> 226 <120> TITLE OF INVENTION: Fatty acid desaturase gene from plants
-> 228 <130> FILE REFERENCE: 50669
-> 228 <130> FILE REFERENCE: 50669
-> 230 <140> CURRENT APPLICATION NUMBER: US 10/069,772A
-> 231 <141> CURRENT FILING DATE: 2002-02-28
-> 233 <160> NUMBER OF SEQ ID NOS: 14
-> 233 <160> NUMBER OF SEQ ID NOS: 14
-> 235 <170> SOFTWARE: PatentIn version 3.3

See error
explanation
on page 5.

This is from sequence 2

Lys Gly Val Phe Trp Tyr His Lys Met
370   375

SEQUENCE LISTING

<110>   Feussner, Ivo
         Hornung, Ellen
         Fritsche, Kathrin
         Peitzsch, Nicola

<120>   Fatty acid desaturase gene from plants

<130>   50669

<140>   US 10/069,772
<141>   2002-02-28

<160>   14

<170>   PatentIn version 3.3

<210>   3
<211>   28
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Primer

<400>   3
ccdrtyttct ctggaarwwh agycaycg

28

This Appeared after Sequence 2.

- Per sequence Rules, show <110> - <170> only at the beginning of the sequence listing.

- Delete <110> - <170> from this section.

```
<210>   6
<211>   27
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Primer


<220>
<221>   misc_feature
<222>   (13)..(13)
<223>   n is inositol

<400>   6
ccartyccay tcngwbgart crtartg                    27
```

(handwritten annotations:) "N" CAN represent only a nucleotide, Not an Alcohol.

Invalid response

pls see item # 13 on error summary sheet.

```
<210>   15
<211>   28
<212>   DNA
<213>  (Artificial Sequence)

<220>
<223>  (none)

<400>   15
tattccaaac ttcttaacaa tccacccg
```

— Pls explain source of genetic material.

Invalid Response

```
<210>   16
<211>   28
<212>   DNA
<213>  (Artificial Sequence)

<220>
<223>  (none)

<400>   16
caattccagt actaggtgta agtgtgtt
```

Same error

See item # 11 on error Summary Sheet,

28

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/24/2006
PATENT APPLICATION: **US/10/069,772A**   TIME: 15:43:06

Input Set : **F:\Feussner-10069772-060211-SEQLIST.txt**
Output Set: **N:\CRF4\02242006\J069772A.raw**

valid Line Length:
e rules require that a line not exceed 72 characters in length. This includes spaces.

```
ɪ#:1;  Line(s)  24,28,29,30,31,32,33,34,36,37,38,39,40,41,42,43,44,45,46,47
ɪ#:1;  Line(s)  48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,67,68
ɪ#:1;  Line(s)  69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88
ɪ#:1;  Line(s)  89,90,91,92,93,94,95,96,97,99,100,101,102,103,104,105,106
ɪ#:1;  Line(s)  107,108,109,110,111,112,113,114,115,116,117,118,119,120,121
ɪ#:1;  Line(s)  122,123,124,125,126,127,128,130,131,132,133
ɪ#:2;  Line(s)  138,139,144,145,146,147,148,149,150,151,152,153,154,155,156
ɪ#:2;  Line(s)  157,158,159,160,161,163,164,165,166,167,168,169,170,171,172
ɪ#:2;  Line(s)  173,174,175,176,177,178,179,180,181,182,183,184,185,186,187
ɪ#:2;  Line(s)  188,189,190,191,192,194,195,196,197,198,199,200,201,202,203
ɪ#:2;  Line(s)  204,205,206,207,208,209,210,211,212,213,214,215
```

VERIFICATION SUMMARY   DATE: 02/24/2006
PATENT APPLICATION: **US/10/069,772A**   TIME: 15:43:06

    Input Set : **F:\Feussner-10069772-060211-SEQLIST.txt**
    Output Set: **N:\CRF4\02242006\J069772A.raw**

```
27 M:282 E: Numeric Field Identifier Missing, <213> is required.
27 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1
219 M:333 E: Wrong sequence grouping, Amino acids not in groups!
219 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:2
219 M:252 E: No. of Seq. differs, <211> LENGTH:Input:377 Found:379 SEQ:2
221 M:280 W: Numeric Identifier already exists, <110> found multiple times
221 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
226 M:280 W: Numeric Identifier already exists, <120> found multiple times
226 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
228 M:280 W: Numeric Identifier already exists, <130> found multiple times
228 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
230 M:280 W: Numeric Identifier already exists, <140> found multiple times
230 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
231 M:280 W: Numeric Identifier already exists, <141> found multiple times
231 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
233 M:280 W: Numeric Identifier already exists, <160> found multiple times
233 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
235 M:280 W: Numeric Identifier already exists, <170> found multiple times
288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
233 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (14) Counted (16)
```